

SEQUENCE LISTING

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NAKANISHI, Hiromi
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<120> Nicotianamine Aminotransferase and Gene Therefor

<130> 2185-0226P

<140> 09/026,400

<141> 1998-02-19

<150> 09-037499 JAPAN

<151> 1997-02-21

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 1660

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (62)..(1444)

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Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala Ala

1

5

10

15

aac ggc aag agc aac ggg cac gcc gcc gcc gcg aac ggc aag agc aac 157

Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn

20

25

30

ggg cac gcg gcg gcg gcg gcg gtg gag tgg aat ttc gcc cgg ggc aag 205

Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys

35

40

45

gac ggc atc ctg gcg acg acg ggg gcg aag aac agc atc cgg gcg ata 253

Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile

50

55

60

cgg tac aag atc agc gcg agc gtg gag gag agc ggg ccg cgg ccc gtg	301
Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val	
65 70 75 80	
ctg ccg ctg gcc cac ggt gac ccg tcc gtg ttc ccg gcc ttc cgc acg	349
Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr	
85 90 95	
gcc gtc gag gcc gaa gac gcc gtc gcc gcc gcg ctg cgc acc ggc cag	397
Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly Gln	
100 105 110	
ttc aac tgc tac gcc gcc ggc gtc ggc ctc ccc gcc gca cga agc gcc	445
Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala	
115 120 125	
gta gca gag cac ttg tca cag ggc gtg ccc tac aag cta tcg gcc gac	493
Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp	
130 135 140	
gac gtc ttc ctc acc gcc ggc gga act cag gcg atc gaa gtc ata atc	541
Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile	
145 150 155 160	
ccg gtg ctg gcc cag act gcc ggc gcc aac ata ctg ctt ccc cgg cca	589
Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro	
165 170 175	
ggc tat cca aat tac gag gcg cga gcg gca ttc aac aag ctg gag gtc	637
Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val	
180 185 190	
cgg cac ttc gac ctc atc ccc gac aag ggg tgg gag atc gac atc gac	685
Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp	
195 200 205	
tcg ctg gaa tcc atc gcc gac aag aac acc acc gcg atg gtc atc ata	733
Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile	
210 215 220	
aac cca aac aat ccg tgc ggc agc gtt tac tcc tac gac cat ctg gcc	781
Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala	
225 230 235 240	
aag gtc gcg gag gtg gca agg aag ctc gga ata ttg gtg atc gct gac	829
Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp	
245 250 255	

TECH CENTER 1600

gag gtt tac ggc aaa ctg gtt ctg ggc agc gcc ccg ttt atc ccg atg	877
Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met	
260 265 270	
ggc gtc ttt ggg cac att gcc ccg gtc ttg tcc att gga tct ctg tcc	925
Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser	
275 280 285	
aag tcg tgg ata gtg cct gga tgg cga ctt gga tgg gtg gcg gtg tac	973
Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr	
290 295 300	
gac ccc aca aag att tta gag aaa act aag atc tct acg tct att acg	1021
Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr	
305 310 315 320	
aat tac ctt aat gtc tca acg gac cca gca acc ttc gtt cag gaa gct	1069
Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala	
325 330 335	
ctt cct aaa att ctt gag aac aca aaa gca gat ttc ttt aag agg att	1117
Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile	
340 345 350	
att ggt cta cta aag gaa tca tca gag ata tgt tat agg gaa ata aag	1165
Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys	
355 360 365	
gaa aac aaa tat att acg tgt cct cac aag cca gaa gga tcg atg ttt	1213
Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe	
370 375 380	
gta atg gtc aaa cta aac tta cat ctt ttg gag gag atc cat gac gac	1261
Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp	
385 390 395 400	
ata gat ttt tgc tgc aag ctc gca aag gaa gaa tca gta att tta tgt	1309
Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys	
405 410 415	
cca ggg agt gtt ctt gga atg gaa aat tgg gtc cgt att act ttt gcc	1357
Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala	
420 425 430	
tgc gtt cca tct tct ctt caa gat gga ctc gaa agg gtc aaa tca ttc	1405
Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe	
435 440 445	

FEB 08 2

TECH CENTER 16

tgt caa agg aac aag aag aag aat tct ata aat ggc tagttgtaca 1454
Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys
450 455 460

caccctagtg tgtacatctg actgaagctg taaatcattt ctagttatcc cccatttata 1514

tatttcaata aaacatattg taatgggttct gttgtagctg tccaagtcac gtactctact 1574

ttttgatgta tttggcctca ttgccttgca tcaatttcaa taaaaatggt tgtgtacacc 1634

aaaaaaaaa aaaaaaaaaa aaaaaa 1660

<210> 2

<211> 461

<212> PRT

<213> Hordeum vulgare

<400> 2

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Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn
20 25 30

Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
35 40 45

Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
50 55 60

Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
65 70 75 80

Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
85 90 95

Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly Gln
100 105 110

Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala
115 120 125

Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp
130 135 140

Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile
145 150 155 160

Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro
 165 170 175

Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val
 180 185 190

Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp
 195 200 205

Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile
 210 215 220

Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala
 225 230 235 240

Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp
 245 250 255

Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met
 260 265 270

Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser
 275 280 285

Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr
 290 295 300

Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr
 305 310 315 320

Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala
 325 330 335

Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile
 340 345 350

Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys
 355 360 365

Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe
 370 375 380

Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
 385 390 395 400

Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
 405 410 415

Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
 420 425 430

Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
 435 440 445

Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys
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<210> 3

<211> 1910

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (76)..(1728)

<400> 3

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 Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala
 1 5 10
 aac ggc ctt gcc gtg gcc gca gcc gcg aac ggc aag agc aac ggc cat 159
 Asn Gly Leu Ala Val Ala Ala Ala Asn Gly Lys Ser Asn Gly His
 15 20 25
 ggc gtg gct gcc gcc gtg aac ggc aag agc aac ggc cat ggc gtg gat 207
 Gly Val Ala Ala Val Asn Gly Lys Ser Asn Gly His Gly Val Asp
 30 35 40
 gcc gac gcg aac ggc aag agc aac ggc cat ggc gtg gct gcc gac gcg 255
 Ala Asp Ala Asn Gly Lys Ser Asn Gly His Gly Val Ala Ala Asp Ala
 45 50 55 60
 aac ggc aag agc aac ggc cat gcc gag gcc act gcg aac ggc cac ggc 303
 Asn Gly Lys Ser Asn Gly His Ala Glu Ala Thr Ala Asn Gly His Gly
 65 70 75
 gag gcc act gcg aac ggc aag acc aac ggc cac cgc gag agc aac ggc 351
 Glu Ala Thr Ala Asn Gly Lys Thr Asn Gly His Arg Glu Ser Asn Gly
 80 85 90
 cat gct gag gcc gcc gac gcg aac ggc gag agc aac gag cat gcc gag 399

His Ala Glu Ala Ala Asp Ala Asn Gly Glu Ser Asn Glu His Ala Glu	
95 100 105	
gac tcc gcg gcg aac ggc gag agc aac ggg cat gcg gcg gcg gcg gca	447
Asp Ser Ala Ala Asn Gly Glu Ser Asn Gly His Ala Ala Ala Ala Ala	
110 115 120	
gag gag gag gag gcg gtg gag tgg aat ttc gcg ggt gcc aag gac ggc	495
Glu Glu Glu Glu Ala Val Glu Trp Asn Phe Ala Gly Ala Lys Asp Gly	
125 130 135 140	
gtg ctg gcg gcg acg ggg gcg aac atg agc atc cgg gcg ata cgg tac	543
Val Leu Ala Ala Thr Gly Ala Asn Met Ser Ile Arg Ala Ile Arg Tyr	
145 150 155	
aag atc agc gcg agc gtg cag gag aag ggg ccg cgg ccc gtg ctg ccg	591
Lys Ile Ser Ala Ser Val Gln Glu Lys Gly Pro Arg Pro Val Leu Pro	
160 165 170	
ctg gcc cac ggg gac ccg tcc gtg ttc ccg gcc ttc cgc acg gcc gtc	639
Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr Ala Val	
175 180 185	
gag gcc gag gac gcc gtc gcc gcc gcc gtg cgc acc ggc cag ttc aac	687
Glu Ala Glu Asp Ala Val Ala Ala Ala Val Arg Thr Gly Gln Phe Asn	
190 195 200	
tgc tac ccc gcc ggc gtc ggc ctc ccc gcc gca cga agc gcc gtg gca	735
Cys Tyr Pro Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala Val Ala	
205 210 215 220	
gag cac ctg tcg cag ggc gtg ccg tac atg cta tcg gcc gac gac gtc	783
Glu His Leu Ser Gln Gly Val Pro Tyr Met Leu Ser Ala Asp Asp Val	
225 230 235	
ttc ctc acc gcc ggc ggg acc cag gcg atc gag gtc ata atc ccg gtg	831
Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile Pro Val	
240 245 250	
ctg gcc cag acc gcc ggc gcc aac att ctg ctc ccc agg cca ggc tac	879
Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro Gly Tyr	
255 260 265	
cca aac tac gag gcg cgc gcc gcg ttc aac agg ctg gag gtc cgg cat	927
Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Arg Leu Glu Val Arg His	
270 275 280	
ttc gac ctc atc ccc gac aag ggg tgg gag atc gac atc gac tcg ctg	975

Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile Asp Asp Asp Ile Asp
480 485 490

ttt tgc tgc aag ctc gca aaa gaa gaa tca gta atc tta tgc cca ggg 1599
Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro Gly
495 500 505

agt gtt ctt gga atg gca aac tgg gtc cgc att act ttt gct tgt gtt 1647
Ser Val Leu Gly Met Ala Asn Trp Val Arg Ile Thr Phe Ala Cys Val
510 515 520

cca tct tct ctt caa gat ggt ctc gga agg atc aaa tca ttc tgt caa 1695
Pro Ser Ser Leu Gln Asp Gly Leu Gly Arg Ile Lys Ser Phe Cys Gln
525 530 535 540

agg aac aag aag aga aat tcg agc gat gat tgc tagttgtata tctgactgaa 1748
Arg Asn Lys Lys Arg Asn Ser Ser Asp Asp Cys
545 550

gctgtaaatc attcccagta tccccatcta tatcttttcaa taaaatggaa ctttttagttc 1808

tctatgaata gaagtcaaca tctccttgaa tatgttctgg ttgttgtggc ctggacgaaa 1868

catagtgaat gttatgttag tgaagttaaa aaaaaaaaaa aa 1910

<210> 4

<211> 551

<212> PRT

<213> Hordeum vulgare

<400> 4

Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala Asn Gly Leu Ala
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Val Ala Ala Ala Ala Asn Gly Lys Ser Asn Gly His Gly Val Ala Ala
20 25 30

Ala Val Asn Gly Lys Ser Asn Gly His Gly Val Asp Ala Asp Ala Asn
35 40 45

Gly Lys Ser Asn Gly His Gly Val Ala Ala Asp Ala Asn Gly Lys Ser
50 55 60

Asn Gly His Ala Glu Ala Thr Ala Asn Gly His Gly Glu Ala Thr Ala
65 70 75 80

Asn Gly Lys Thr Asn Gly His Arg Glu Ser Asn Gly His Ala Glu Ala

Ala Asp Ala Asn Gly Glu Ser Asn Glu His Ala Glu Asp Ser Ala Ala
100 105 110

Asn Gly Glu Ser Asn Gly His Ala Ala Ala Ala Glu Glu Glu Glu
115 120 125

Ala Val Glu Trp Asn Phe Ala Gly Ala Lys Asp Gly Val Leu Ala Ala
130 135 140

Thr Gly Ala Asn Met Ser Ile Arg Ala Ile Arg Tyr Lys Ile Ser Ala
145 150 155 160

Ser Val Gln Glu Lys Gly Pro Arg Pro Val Leu Pro Leu Ala His Gly
165 170 175

Asp Pro Ser Val Phe Pro Ala Phe Arg Thr Ala Val Glu Ala Glu Asp
180 185 190

Ala Val Ala Ala Ala Val Arg Thr Gly Gln Phe Asn Cys Tyr Pro Ala
195 200 205

Gly Val Gly Leu Pro Ala Ala Arg Ser Ala Val Ala Glu His Leu Ser
210 215 220

Gln Gly Val Pro Tyr Met Leu Ser Ala Asp Asp Val Phe Leu Thr Ala
225 230 235 240

Gly Gly Thr Gln Ala Ile Glu Val Ile Ile Pro Val Leu Ala Gln Thr
245 250 255

Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro Gly Tyr Pro Asn Tyr Glu
260 265 270

Ala Arg Ala Ala Phe Asn Arg Leu Glu Val Arg His Phe Asp Leu Ile
275 280 285

Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp Ser Leu Glu Ser Ile Ala
290 295 300

Asp Lys Asn Thr Thr Ala Met Val Ile Ile Asn Pro Asn Asn Pro Cys
305 310 315 320

Gly Ser Val Tyr Ser Tyr Asp His Leu Ser Lys Val Ala Glu Val Ala
325 330 335

Lys Arg Leu Gly Ile Leu Val Ile Ala Asp Glu Val Tyr Gly Lys Leu

<223> Description of Artificial Sequence:primer 1

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<221> modified_base

<222> (1)..(23)

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23

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer 2

<220>

<221> modified_base

<222> (1)..(20)

<223> n=inosine

<400> 6

gcdatrtgnc craanacncc

20

<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:dt17 adapter
primer

<400> 7

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